



California Science Center
CALIFORNIA STATE SCIENCE FAIR
2001 PROJECT SUMMARY

Your Name (List all student names if multiple authors.) Tom J. Maddock	Science Fair Use Only S0320
Project Title (Limit: 120 characters. Those beyond 120 will be ignored. See pg. 9) Hydrogen Bonding in Proteins	Division _ Junior (6-8) <u>X</u> Senior (9-12)
Preferred Category (See page 5 for descriptions.) 3 - Biochemistry / Molecular Biology	
Abstract (Include Objective, Methods, Results, Conclusion. See samples on page 14.) Use no attachments. Only text inside these boxes will be used for category assignment or given to your judges.	
<p>Objective: In my project, I attempt to determine exactly what role hydrogen bonding plays in the formation of the secondary and tertiary structures proteins are known to have.</p> <p>Materials and Methods: I decided early on that, to accomplish this objective, I would create a computer program capable of accurately simulating the properties of a protein involved in hydrogen bond formation. Thus, my first steps were largely research. I spent months on the Internet studying information about protein formation, hydrogen bonding, electronegativity, and other related topics. Then, once I felt I had become sufficiently educated, I set out creating the program. I chose to write the program in the C++ programming language because its unique object-oriented architecture allowed me to easily construct virtual atoms and molecules that I could manipulate and join together within the program. Once the program was finished, I had it simulate many molecules ranging from simple amino acids to larger, complete proteins.</p> <p>Results: From the data returned by the program, I was able to determine the "hot spots" along the protein that would tend to attract, and thus pull the molecule into a specific conformation. In the proteins tested, I saw a very consistent repeating pattern of opposite charges in atoms along the nitrogen-carbon-carbon backbone. The oxygen double bonded to every third carbon exhibited a highly positive charge, while the hydrogen bonded to the succeeding nitrogen exhibited a highly negative charge. These charges were easily strong enough to cause a major contortion in the shape of the molecule, if they formed a hydrogen bond. In all the polypeptides sampled, ranging from 3 to over 70 amino acids, this was evident.</p> <p>Conclusions: After analyzing the repeating pattern of opposite charges, I concluded that it did, undoubtedly, have a substantial influence on a protein's three-dimensional shape. When present in polypeptides of even minimal length, this pattern easily supported the formation of an alpha helix or beta-pleated sheet, provided the molecule was flexible enough to allow it. Now, since I understand that hydrogen bonding along the backbone of a protein influences its secondary structure formation, I can safely say I accomplished my objective, and was hopefully able to move us one step closer towards our goal of predicting a protein's structure.</p>	
Summary Statement (In one sentence, state what your project is about.) Through using a computer program of my own design, I attempt to discover what role hydrogen bonding plays in the determination of a protein's shape.	
Help Received in Doing Project (e.g. Mother helped type report; Neighbor helped wire board; Used lab equipment at university X under the supervision of Dr. Y; Participant in NSF Young Scholars Program) See Display Regulation #8 on page 4. My uncle helped me locate memory and syntax errors in the program. I received help from my mother in the layout and design of the project display.	